Approved 7/3/03 PP

ACTGTCTGGAACTGGACTGAGTCACCAAAAGGCGAATGGCTTCATCTTATAAAATGTCTGAACAAAGCACA
ACTTCTGAGCACATTTTACAGAAGACATGTGATCACCTGATCCTGACTAACCGTTCTGGATTAGAGACAGA
CTCAGTAGCAGAGGAAATGAAGCAGACTGTGGAGGGACAGGGGCATACAGTGCACTGGGCAGCTCTCCTGA
TACTCGCGGTGATAATACCCACCATTGGTGGGAACATCCTTGTGATTCTGGCTGTTGCACTGGAGAAAAGG
CTGCAGTACGCTACCAACTACTTTTTAATGTCCTTGGCGATAGCAGATTTGCTGGTTGGATTGTTTGTGAT
GCCGATTGCCCTCTTGACAATCATGTTTGAGGCTATATGGCCCCTCCCACTGGCCCTGTGTCCTGCCTGGT
TATTCCTCGATGTTCTCTTTTCAACTGCCTCCATCATGCATCTCTGTGCCATTTCCCTGGACCGCTATATA
GCCATCAAAAAGCCAATTCAGGCCAATCAGTGCAACACCCGGGCTACTGCATTCATCAAGATTACAGTGGT
ATGGTTAATTTCAATAGGCATCGCCATCCCAGTCCCTATTAAAGGAATCGAGACTGATGTGATTAATCCAC
ACAATGTCACCTGTGAGCTGACAAAGGACCGCTTTGGCAGTTTTATGGTCTTTGGGTCACTGGCTGCTTTC
TTCGTACCTCTCACCATCATGGTAGTCACTTACTTTCTCACCATTCACACTTTACAGAAGAAAGCTTACTT
GGTCAAAAATAAGCCACCTCAACGCCTAACACGGTGGACTGTGCCCACAGTTTTCCTAAGGGAAGACTCAT
CCTTTTCATCACCAGAAAAGGTGGCAATGCTGGATGGGTCTCACAGGGATAAAATTCTACCTAACTCAAGT
GATGAGACACTTATGCGAAGAATGTCCTCAGTTGGAAAAAGATCAGCCCAAACCATTTCTAATGAGCAGAG
AGCCTCGAAGGCCCTTGGAGTCGTGTTTTTCCTTTTTCTGCTTATGTGGTGCCCCTTTTTTATTACAAATC
TAACTTTAGCTCTGTGTGATTCCTGCAATCAGACCACTCTCAAAACACTCCTGGAGATATTTGTGTGGATA
GGCTACGTTTCCTCGGGGGTGAATCCTCTGATCTATACACTCTTCAATAAGACATTTCGGGAAGCATTTGG
CAGGTACATCACCTGCAATTACCGAGCCACAAAGTCAGTAAAAGCACTTAGGAAGTTTTCCAGTACACTTT
GTTTTGGGAATTCAATGGTAGAAAACTCTAAATTTTTCACAAAACATGGAATTCGAAATGGGATCAACCCT
GCCATGTACCAGAGCCCAATGAGGCTCCGATGTTCAACCATTCAGTCCTCATCAATCATCCTCCTCGATAC
CCTTCTCACTGAAAACGATGGCGACAAAGCGGAAGAGCAGGTCAGCTACATATTGCAGGAACGGGCCGGCC
TCATCTTGAGAGAGGGTGATGAGCAGGACGCACGCGCACCATGGCAGGTTCAAGAGTGA (SEQ ID NO:1)

MASSYKMSEQSTTSEHILQKTCDHLILTNRSGLETDSVAEEMKQTVEGQGHTVHWAALLILAVIIPTIGGN
ILVILAVALEKRLQYATNYFLMSLAIADLLVGLFVMPIALLTIMFEAIWPLPLALCPAWLFLDVLFSTASI
MHLCAISLDRYIAIKKPIQANQCNTRATAFIKITVVWLISIGIAIPVPIKGIETDVINPHNVTCELTKDRF
GSFMVFGSLAAFFVPLTIMVVTYFLTIHTLQKKAYLVKNKPPQRLTRWTVPTVFLREDSSFSSPEKVAMLD
GSHRDKILPNSSDETLMRRMSSVGKRSAQTISNEQRASKALGVVFFLFLLMWCPFFITNLTLALCDSCNQT
TLKTLLEIFVWIGYVSSGVNPLIYTLFNKTFREAFGRYITCNYRATKSVKALRKFSSTLCFGNSMVENSKF
FTKHGIRNGINPAMYQSPMRLRCSTIQSSSIILLDTLLTENDGDKAEEQVSYILQERAGLILREGDEQDAR
APWQVQE (SEQ ID NO:2)

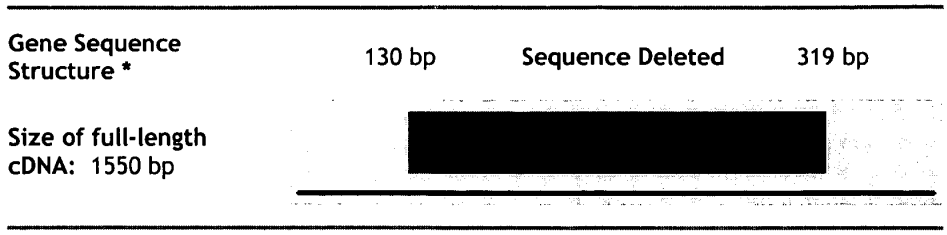
FIGURE 1

Underlined = deleted in targeting construct

Bold = sequence flanking Neo insert in targeting construct

ACTGTCTGGAACTGGACTGAGTCACCAAAAGGCGAATGGCTTCATCTTATAAAATGTCTG
AACAAAGCACAACTTCTGAGCACATTTTACAGAAGACATGTGATCACCTGATCCTGACTA
ACCGTTCTGGATTAGAGACAGACTCAGTAGCAGAGGAAATGAAGCAGACTGTGGAGGGAC
AGGGGCATACAGTGCACTGGGCAGCTCTCCTGATACTCGCGGTGATAATACCCACCATTG
GTGGGAACATCCTTGTGATTCTGGCTGTTGCACTGGAGAAAAGGCTGCAGTACGCTACCA
ACTACTTTTTAATGTCCTT **GGCGATAGCAGATTTGCTGGTTGGATTGTTTGTGATGCCGA**
TTGCCCTCTTGACAATCATGTTTGAGGCTATATGGCCCCTCCCACTGGCCCTGTGTCCTG
CCTGGTTATTCCTCGATGTTCTCTTTTCAACTGCCTCCATCATGCATCTCTGTGCCATTT
CCCTGGACCGCTATATAGCCATCAAAAAGCCAATTCAGGCCAATCAGTGCAACACCCGGG
CTACTGCATTCATCAAGATTACAGTGGTATGGTTAATTTCAATAGGCATCGCCATCCCAG
TCCCTATTAAAGGAATCGAGACTGATGTGATTAATCCACACAATGTCACCTGTGAGCTGA
CAAAGGACCGCTTTGGCAGTTTTATGGTCTTTGGGTCACTGGCTGCTTTCTTCGTACCTC
TCACCATCATGGTAGTCACTTACTTTCTCACCATTCACACTTTACAGAAGAAAGCTTACT
TGGTCAAAAATAAGCCACCTCAACGCCTAACACGGTGGACTGTGCCCACAGTTTTCCTAA
GGGAAGACTCATCCTTTTCATCACCAGAAAAGGTGGCAATGCTGGATGGGTCTCACAGGG
ATAAAATTCTACCTAACTCAAGTGATGAGACACTTATGCGAAGAATGTCCTCAGTTGGAA
AAAGATCAGCCCAAACCATTTCTAATGAGCAGAGAGCCTCGAAGGCCCTTGGAGTCGTGT
TTTTCCTTTTTCTGCTTATGTGGTGCCCCTTTTTTATTACAAATCTAACTTTAGCTCTGT
GTGATTCCTGCAATCAGACCACTCTCAAAACACTCCTGGAGATATTTGTGTGGATAGGCT
ACGTTTCCTCGGGGGTGAATCCTCTGATCTATACACTCTTCAATAAGACATTTCGGGAAG
CATTTGGCAGGTACATCACCTGCAATTACCGAGCCACAAAGTCAGTAAAAGCACTTAGGA
AGTTTTCCAGTACACTTTGTTTTGGGAATTCAATGGTAGAAAACTCTAAATTTTTCACAA
AACATGGAATTCGAAATGGGATCAACCCTGCCATGTACCAGAGCCCAATGAGGCTCCGAT
GTTCAACCATTCAGTCCTCATCAATCATCCTCCTCGATACCCTTCTCACTGAAAACGATG
GCGACAAAGCGGAAGAGCAGGTCAGCTACATATTGCAGGAACGGGCCGGCCTCATCTTGA
GAGAGGGTGATGAGCAGGACGCACGCGCACCATGGCAGGTTCAAGAGTGA

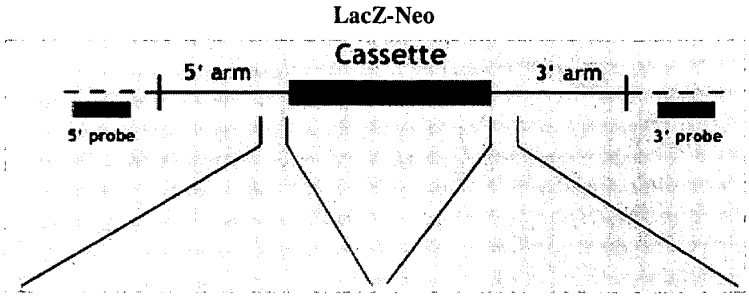
FIGURE 2A



Targeting Vector* (genomic sequence)

Construct Number: 2520

Arm Length:
5': 1.6 kb
3': 5 kb



Targeting Vector
Endogenous Locus

* Not drawn to scale

5'>TGAGTGTCTGGTGGGTTTGCT AAATGCTTTGCTAAAGCAGATGAC TTGCTTAGCTACTGACCATGCTGA CCACTGTCTGGAACTGGACTGAGT CACCAAAAGGCGAATGGCTTCATC TTATAAAATGTCTGAACAAAGCAC AACTTCTGAGCACATTTTACAGAA GACATGTGATCACCTGATCCTGAC TAACCGTTCTG<3' (SEQ ID NO:3)	5'>GGCGATAGCAGATTTGCTGGT TGGATTGTTTGTGATGCCGATTGC CCTCTTGACAATCATGTTTGGTGA GTATTTCCCCTTGTTCCTGCCACT GAACACTACTAACGTAGTGAAATG GACACTCACTGACCTTTATTTTGT TTGAAATAAAAGAAGGACCTGGAT TAAAAACACAGAAGGGAACATTCC TTCATTTTTCA<3' (SEQ ID NO:4)

FIGURE 2B